

A protein - protein search, using Bw model					
Run on: November 6, 2004, 19:24:00 ; Search time 66.875 Seconds (without alignment) ; 43.019 Million cell updates/sec					
Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	48	Q41032	Q41032 pism sat
2	27	100.0	51	Q8QV41	Q8QV41 avian rec
3	27	100.0	51	Q8QV42	Q8QV42 avian rec
4	27	100.0	51	Q8QV43	Q8QV43 avian rec
5	27	100.0	51	Q8QV46	Q8QV46 avian rec
6	27	100.0	51	Q8QV47	Q8QV47 avian rec
7	27	100.0	51	Q8QV48	Q8QV48 avian rec
8	27	100.0	51	Q8QV51	Q8QV51 avian rec
9	27	100.0	51	Q8QV52	Q8QV52 avian rec
10	27	100.0	51	Q8QV53	Q8QV53 avian rec
11	27	100.0	51	Q8QV55	Q8QV55 avian rec
12	27	100.0	91	Q8BT47	Q8BT47 lactobac
13	27	100.0	97	Q6MNH8	Q6MNH8 bdellov
14	27	100.0	97	CAE79173	CAE79173 bdellov
15	27	100.0	104	Q6LHW8	Q6LHW8 photob
16	27	100.0	104	CAG23112	CAG23112 photob
17	27	100.0	108	Q32358	Q32358 campylob
18	27	100.0	114	Q59363	Q59363 pyrococ
19	27	100.0	136	Q43672	Q43672 vicia fal
20	27	100.0	138	Q7X116	Q7X116 leptosp
21	27	100.0	142	Q6QR05	Q6QR05 uncultu
22	27	100.0	142	AS19404	AS19404 uncultu
23	27	100.0	159	Q8G7N6	Q8G7N6 bifidobac
24	27	100.0	167	Q9AVD4	Q9AVD4 nicotian
25	27	100.0	174	Q64683	Q64683 mesocr
26	27	100.0	181	Q744N3	Q744N3 mycobac
27	27	100.0	181	Q72SJ2	Q72SJ2 leptosp
28	27	100.0	188	Q8F318	Q8F318 leptosp
29	27	100.0	188	Q8H7H3	Q8H7H3 arabidop
30	27	100.0	190	Q869990	Q869990 leprosi
31	27	100.0	198	Q8H7H3	Q8H7H3 arabidop

32	27	100.0	193	2	Q8GBS3	treponema	m
33	27	100.0	195	2	Q7U656	synchrocc	
34	27	100.0	197	1	ENGB_ARCFU	archaeoglob	
35	27	100.0	201	2	Q54257	streptomyce	
36	27	100.0	205	2	Q52806	amycolatops	
	37	100.0	205	2	Q939X4	amycolatops	
	38	100.0	206	2	Q8JWF8	streptomyce	
	39	100.0	207	2	Q7XTL9	oryza sativ	
	40	100.0	208	2	Q9PH00	halobacteri	
	41	100.0	237	2	Q8NL18	corynebacte	
	42	100.0	239	2	Q73mb8	treponema	d
	43	100.0	239	2	AAS12158	treponema	
	44	100.0	244	1	THIX_PYRAE	pyraculum	
	45	100.0	247	2	Q89uWd	bradyrhizob	

RESULT 1						
Q41032		PRELIMINARY;	PRT;	48	AA.	
ID	Q41032;					
AC	Q41032;					
DT	01-NOV-1996	(TREMBLrel.)	01,	Created)		
	DT	01-NOV-1996	(TREMBLrel.)	01,	Last sequence update)	
	DT	01-JUN-2003	(TREMBLrel.)	24,	Last annotation update)	
DB	Legumin J	(Fragment).				
OS	Pisum sativum	(Garden pea).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
CC	Spermatophytina; Magnoliopsida; eudicotyledons; core eudicots; rosids;					
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Viciae; Pileum.					
OX	NCBI_TaxID:3888;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MBIDLINE=87080257;	PubMed=2431897;				
RA	Brown J.W.S., Peix G., Frandewey D.;					
RA	"Accurate <i>in vitro</i> splicing of two pre-mRNA plant introns in a HeLa					
RT	cell1 nuclear extract.",					
RT	cell1 nuclear extract.",					
RL	EMBO J. 5:749-2758(1986).					
DR	EMBL: M26771; AAA333674.1; -.					
DR	PIR: T06450; T06450.					
FT	NON_TER	1	1			
FT	NON_TER	48	48			
SQ	SEQUENCE	48 AA;	5608 MW;	0DAB5F0AF6A7BD9 CRC64;		
Query	Match	100.0%	Score 27;	DB 2;	Length 48;	
Best	Local Similarity	100.0%;	Pred No. 60;			
Matches	5;	Conservative	0;	Mismatches	0;	Gaps
Qy	1	TPRVF 5				
Db	14	TPRVF 18				
RESULT 2						
Q8QV41		PRELIMINARY;	PRT;	51	AA.	
ID	Q8QV41;					
AC	Q8QV41;					
DT	01-JUN-2002	(TREMBLrel.)	21,	Created)		
	DT	01-JUN-2002	(TREMBLrel.)	21,	Last sequence update)	
	DT	01-JUN-2003	(TREMBLrel.)	24,	Last annotation update)	
DE	Sigma C protein (Fragment).					
OS	Avian reovirus NUL19_97M.					
OC	Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.					
OX	NCBI_TaxID:17325;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=NUL19_97M;					
RA	Kanc A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,					
RA	ter Haarne A.;					
RA	Submitted (PEB-2001) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AF34196; AAL83467.1;					
DR	InterPro: IPR007652; Reo_sigmaC.					

DR	PFAM; PF04582; Reo_sigmaC; 1.	Qy	1 TPRVF 5 []	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 5
FT	NON-TER 1				Q8QV46 PRELIMINARY; PRT; 51 AA.
FT	NON-TER 51				AC Q8QV46; DT 01-JUN-2002 (TREMBLrel. 21, Created)
FT	NON-SEQUENCE 51 AA;				DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
SQ	5660 MW;				DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
	4A0FE823ED41C0C4 CRC64;				DE Sigma C protein (Fragment).
					OS Avian reovirus NIA10 96M.
					OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
					OX NCBI_TaxID=177320;
					RN [1];
					RP SEQUENCE FROM N.A.
					RC STRAIN=NIA10 96M;
					RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,
					RA ter Huurne A.;
					RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
					RL EMBL; AP354195; AAL83466 1; -
					DR InterPro; IPR007662; Reo_sigmaC.
					DR Pfam; PF04582; Reo_sigmaC; 1.
					FT NON-TER 51
					FT NON-TER 51
					FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;
					FT 34 TPRVF 38
					DR 34 TPRVF 38
Qy	1 TPRVF 5 []	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 3	Q8QV42 PRELIMINARY; PRT; 51 AA.	Q8QV42 PRELIMINARY; PRT; 51 AA.
Db	34 TPRVF 38			AC Q8QV42; DT 01-JUN-2002 (TREMBLrel. 21, Created)	AC Q8QV42; DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
				DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
				DB Sigma C protein (Fragment).	DB Sigma C protein (Fragment).
				OS Avian reovirus NIA10 80M.	OS Avian reovirus NIA10 80M.
				OC dsRNA viruses; Reoviridae; Orthoreovirus.	OC dsRNA viruses; Reoviridae; Orthoreovirus.
				RN NCBI_TaxID=177324;	RN NCBI_TaxID=177324;
				RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,	RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,
				RA ter Huurne A.;	RA ter Huurne A.;
				RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
				RL EMBL; AP354195; AAL83466 1; -	RL EMBL; AP354195; AAL83466 1; -
				DR InterPro; IPR007662; Reo_sigmaC.	DR InterPro; IPR007662; Reo_sigmaC.
				DR Pfam; PF04582; Reo_sigmaC; 1.	DR Pfam; PF04582; Reo_sigmaC; 1.
				FT NON-TER 51	FT NON-TER 51
				FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;	FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;
				FT 34 TPRVF 38	FT 34 TPRVF 38
Qy	1 TPRVF 5 []	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 6	Q8QV47 PRELIMINARY; PRT; 51 AA.	Q8QV47 PRELIMINARY; PRT; 51 AA.
Db	34 TPRVF 38			AC Q8QV47; DT 01-JUN-2002 (TREMBLrel. 21, Created)	AC Q8QV47; DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
				DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
				DB Sigma C protein (Fragment).	DB Sigma C protein (Fragment).
				OS Avian reovirus NIA08 96M.	OS Avian reovirus NIA08 96M.
				OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.	OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
				OX NCBI_TaxID=177319;	OX NCBI_TaxID=177319;
				RN [1];	RN [1];
				RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
				RC STRAIN=NIA08 96M;	RC STRAIN=NIA08 96M;
				RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,	RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,
				RA ter Huurne A.;	RA ter Huurne A.;
				RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
				RL EMBL; AP354195; AAL83461 1; -	RL EMBL; AP354195; AAL83461 1; -
				DR InterPro; IPR007662; Reo_sigmaC.	DR InterPro; IPR007662; Reo_sigmaC.
				DR Pfam; PF04582; Reo_sigmaC; 1.	DR Pfam; PF04582; Reo_sigmaC; 1.
				FT NON-TER 51	FT NON-TER 51
				FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;	FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;
				FT 34 TPRVF 38	FT 34 TPRVF 38
Qy	1 TPRVF 5 []	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 4	Q8QV43 PRELIMINARY; PRT; 51 AA.	Q8QV43 PRELIMINARY; PRT; 51 AA.
Db	34 TPRVF 38			AC Q8QV43; DT 01-JUN-2002 (TREMBLrel. 21, Created)	AC Q8QV43; DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
				DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
				DB Sigma C protein (Fragment).	DB Sigma C protein (Fragment).
				OS Avian reovirus NIA18 97M.	OS Avian reovirus NIA18 97M.
				OC dsRNA viruses; Reoviridae; Orthoreovirus.	OC dsRNA viruses; Reoviridae; Orthoreovirus.
				NCBI_TaxID=177323;	NCBI_TaxID=177323;
				RN [1];	RN [1];
				RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
				RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,	RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,
				RA ter Huurne A.;	RA ter Huurne A.;
				RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
				RL EMBL; AP354194; AAL83465 1; -	RL EMBL; AP354194; AAL83465 1; -
				DR InterPro; IPR007662; Reo_sigmaC.	DR InterPro; IPR007662; Reo_sigmaC.
				DR Pfam; PF04582; Reo_sigmaC; 1.	DR Pfam; PF04582; Reo_sigmaC; 1.
				FT NON-TER 51	FT NON-TER 51
				FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;	FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;
				FT 34 TPRVF 38	FT 34 TPRVF 38
Qy	1 TPRVF 5 []	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 5	Q8QV46 PRELIMINARY; PRT; 51 AA.	Q8QV46 PRELIMINARY; PRT; 51 AA.
Db	34 TPRVF 38			AC Q8QV46; DT 01-JUN-2002 (TREMBLrel. 21, Created)	AC Q8QV46; DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
				DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
				DB Sigma C protein (Fragment).	DB Sigma C protein (Fragment).
				OS Avian reovirus NIA10 96M.	OS Avian reovirus NIA10 96M.
				OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.	OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
				OX NCBI_TaxID=177320;	OX NCBI_TaxID=177320;
				RN [1];	RN [1];
				RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
				RC STRAIN=NIA10 96M;	RC STRAIN=NIA10 96M;
				RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,	RA Kant A.; Balk F.; Born L.; van Roozelaar D.; Heijmans J.; Gielkens A.,
				RA ter Huurne A.;	RA ter Huurne A.;
				RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
				RL EMBL; AP354193; AAL83466 1; -	RL EMBL; AP354193; AAL83466 1; -
				DR InterPro; IPR007662; Reo_sigmaC.	DR InterPro; IPR007662; Reo_sigmaC.
				DR Pfam; PF04582; Reo_sigmaC; 1.	DR Pfam; PF04582; Reo_sigmaC; 1.
				FT NON-TER 51	FT NON-TER 51
				FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;	FT NON-TER 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;
				FT 34 TPRVF 38	FT 34 TPRVF 38

RESULT 7	Q8QV48	PRELIMINARY;	PRT;	51 AA.
AC	Q8QV48;			
DT	01-JUN-2002	(TREMBLrel. 21, Created)		
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Sigma C protein (Fragment).			
OS	Avian reovirus NLA07 96M.			
OC	dsRNA viruses; Reoviridae; Orthoreovirus.			
NCBI_TaxID	177318;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NLNA07 97M;			
RA	Kant A., Balk F., Born L., van Roodzaelaar D., Heijmans J., Gielkens A., ter Huurne A.;			
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
EMBL	AF354185; AAL83456.1;			
DR	IPR007662; Reo_sigmaC; 1.			
InterPro	PF04582; Reo_sigmaC; 1.			
PFAM	PF04582; Reo_sigmaC; 1.			
Qy	1 TPRVF 5			
Db	34 TPRVF 38			
RESULT 8	Q8QV51	PRELIMINARY;	PRT;	51 AA.
AC	Q8QV51;			
DT	01-JUN-2002	(TREMBLrel. 21, Created)		
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Sigma C protein (Fragment).			
OS	Avian reovirus GBLO8 97M.			
OC	dsRNA viruses; Reoviridae; Orthoreovirus.			
NCBI_TaxID	177315;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kant A., Balk F., Born L., van Roodzaelaar D., Heijmans J., Gielkens A., ter Huurne A.;			
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
EMBL	AF354186; AAL83457.1;			
DR	IPR007662; Reo_sigmaC; 1.			
InterPro	PF04582; Reo_sigmaC; 1.			
PFAM	PF04582; Reo_sigmaC; 1.			
FT	NON-TER 1			
NON-TER	51			
SEQUENCE	51 AA; 5660 MW;	4A0FE823ED41C0C4 CRC64;		
Qy	1 TPRVF 5			
Db	34 TPRVF 38			
RESULT 10	Q8QV53	PRELIMINARY;	PRT;	51 AA.
AC	Q8QV53;			
ID	[1]			
Q8QV53				
PRELIMINARY;				
PT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Sigma C protein (Fragment).			
OS	Avian reovirus GBLO4 97T.			
NCBI_TaxID	177313;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GBLO4 97T;			
RA	Kant A., Balk F., Born L., van Roodzaelaar D., Heijmans J., Gielkens A., ter Huurne A.;			
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
EMBL	AF354184; AAL83455.1;			
DR	IPR007662; Reo_sigmaC; 1.			
InterPro	PF04582; Reo_sigmaC; 1.			
PFAM	PF04582; Reo_sigmaC; 1.			
FT	NON-TER 1			
NON-TER	51			
SEQUENCE	51 AA; 5632 MW;	4A0FE823ED57B1A3 CRC64;		
Qy	1 TPRVF 5			
Db	34 TPRVF 38			
RESULT 11	Q8QV55	PRELIMINARY;	PRT;	51 AA.
AC	Q8QV55;			
ID	[1]			
Q8QV55				
PRELIMINARY;				
PT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Sigma C protein (Fragment).			
OS	Avian reovirus GB11 97M.			
NCBI_TaxID	177311;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GE11 97M;			
RA	Kant A., Balk F., Born L., van Roodzaelaar D., Heijmans J., Gielkens A., ter Huurne A.;			
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
EMBL	AF354186; AAL83457.1;			
DR	IPR007662; Reo_sigmaC; 1.			
InterPro	PF04582; Reo_sigmaC; 1.			
PFAM	PF04582; Reo_sigmaC; 1.			
FT	NON-TER 1			
NON-TER	51			
SEQUENCE	51 AA; 5660 MW;	4A0FE823ED41C0C4 CRC64;		
Qy	1 TPRVF 5			
Db	34 TPRVF 38			
RESULT 9	Q8QV52	PRELIMINARY;	PRT;	51 AA.
AC	Q8QV52;			
ID	[1]			
Q8QV52				
PRELIMINARY;				
PT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Sigma C protein (Fragment).			
OS	Avian reovirus GE11 97M.			
NCBI_TaxID	177311;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GE11 97M;			
RA	Kant A., Balk F., Born L., van Roodzaelaar D., Heijmans J., Gielkens A., ter Huurne A.;			
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
EMBL	AF354186; AAL83457.1;			
DR	IPR007662; Reo_sigmaC; 1.			
InterPro	PF04582; Reo_sigmaC; 1.			
PFAM	PF04582; Reo_sigmaC; 1.			
FT	NON-TER 1			
NON-TER	51			
SEQUENCE	51 AA; 5660 MW;	4A0FE823ED41C0C4 CRC64;		
Qy	1 TPRVF 5			
Db	34 TPRVF 38			

RN	Kant A., Balk F., Born L., van Roozeelaar D., Heijmans J., Gielkens A., ter Huurne A.; Submitted (PFB-2/2001) to the EMBL/Genbank/DDBJ databases.	RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F., RA Sockelt R.E., Schuster S.C.; "A predator unmasked: life cycle of <i>Bdellovibrio bacteriovorus</i> from a genomic perspective." RA Science 303:689-692 (2004).
DR	EMBL: FJ354182; DAL83453.1; -.	RT DR
DR	InterPro; IPR007662; Reo_sigmaC.	RT DR
DR	Protein; PF04582; Reo_sigmaC; 1.	RT DR
FT	NON-TER 1 1	RT DR
FT	NON-TER 51 51	RT DR
SEQ	SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41CC04 CRC64;	DR InterPro; IPR007341; Transgly_assoc.
		KW PFam; PF04226; Transgly_assoc; 1.
		KW Complete proteome.
		KW Sequence 97 AA; 10712 MW; F3CB159308976941 CRC64;
SQ		SEQUENCE 97 AA; 10712 MW; F3CB159308976941 CRC64;
RESULT 12		
Q88T47	Query Match 100.0%; Score 27; DB 2; Length 51; Best Local Similarity 100.0%; Pred. No. 63; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 100.0%; Score 27; DB 2; Length 97; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 TPRVF 5	Qy 1 TPRVF 5
Db	34 TPRVF 36	Db 60 TPRVF 64
RESULT 13		
Q88T47	PRELIMINARY; PRT; 91 AA.	RESULT 14
AC Q88T47;	AC CAE79173	AC CAE79173
DT 01-JUN-2003 (TREMBLrel. 24, Created)	ID CAE79173;	ID CAE79173;
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)	AC CAE79173;	AC CAE79173;
DR 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT 02-MAR-2004 (TREMBLrel. 27, Created)	DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein 3141.	DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)	DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
GN OrderedLocusNames=3141;	DE Transglycosylase associated protein.	DE BD1276.
OS Lactobacillus plantarum.	GN	OS Bdellovibrio bacteriovorus.
OC Firmicutes; Lactobacillales; Lactobacillaceae;	OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;	OC Bdellovibrionaceae; Bdellovibrio.
OC Lactobacillus.		NCBI_TaxID=959;
OX NCBI_TaxID=1590;		RN [1]
RN		RP SEQUENCE FROM N.A.
RC PRELIMINARY;		RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RD 12566566; PubMed=12566566;		RD PubMed=14752164;
RX WCF51; MEDLINE=2248096; PubMed=12566566;		RX
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Sandbrink H.M., Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M., Fiers M.W.E.J., Strickema W., Klein Bankhorst R.M., Bron P.A., Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B., De Vos W.M., Siezen R.J.; "Complete genome sequence of <i>Lactobacillus plantarum</i> WCF51."; RR Proc. Natl. Acad. Sci. U.S.A. 100:1930-1935 (2003).	RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F., RA Sockelt R.E., Schuster S.C.; "A predator unmasked: life cycle of <i>Bdellovibrio bacteriovorus</i> from a genomic perspective." RA Science 303:689-692 (2004).	
RL EMBL: BX842649; CDD65103.1; -.	RL DR EMBL: BX842649; CAE79173.1; -.	
KW Complete proteome; Hypothetical protein.	RL Sequence 97 AA; 10712 MW; F3CB159308976941 CRC64;	
SEQ SEQUENCE 91 AA; 10638 MW; 1589F036EB5A9D CRC64;	SEQ	
RESULT 14		
Q6LNHW8	Query Match 100.0%; Score 27; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 100.0%; Score 27; DB 2; Length 97; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC Q6LNHW8;	AC Q6LNHW8	AC Q6LNHW8
DT 05-JUL-2004 (TREMBLrel. 27, Created)	ID Q6LNHW8;	ID Q6LNHW8;
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	AC Q6LNHW8;	AC Q6LNHW8;
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Transglycosylase associated protein.	DE Hypothetical protein.	DE Hypothetical protein.
GN OrderedLocusNames=Bd1276;	GN OrderedLocusNames=PBRB1240;	GN Photobacterium profundum (Photobacterium sp. (strain SS9)).
OS Bdellovibrio bacteriovorus.	OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	OC Vibrionaceae; Photobacterium.
OC Bacteria; Protobacteria; Deltaproteobacteria; Bdellovibrionales;	OC	NCBI_TaxID=4109;
OC Bdellovibrionaceae; Bdellovibrio.		RN [1]
RN SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;		RC RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., RA .Cestaro A., Malacrida G., Simonato B., Cannata N., Bartlett D., RA
RX PubMed=14752164;		RX

RA Valle G.; analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.",
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CP378678; CAG23112.1;
KW Complete proteome; Hypothetical protein,
SQ SEQUENCE 104 AA; 11783 MW; 5679626687769163 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 104;
Best Local Similarity 100.0%; Prd. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVP 5
Db 86 TPRVP 90

Search completed: November 6, 2004, 19:52:56
Job time : 69.875 secs

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